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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,706

DATE: 11/14/2001
TIME: 14:12:30

Input Set : A:\55871965.app
Output Set: N:\CRF3\11142001\I830706.raw

4 <110> APPLICANT: TOJI, SHINGO
5 YANO, MINORU
6 TAMAI, KATSUYUKI
8 <120> TITLE OF INVENTION: THIOREDOXIN REDUCTASE II
10 <130> FILE REFERENCE: 55865-71965
12 <140> CURRENT APPLICATION NUMBER: 09/830,706
13 <141> CURRENT FILING DATE: 2001-04-27
15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05983
16 <151> PRIOR FILING DATE: 1999-10-28
18 <150> PRIOR APPLICATION NUMBER: JP 1998-310422
19 <151> PRIOR FILING DATE: 1998-10-30
21 <160> NUMBER OF SEQ ID NOS: 38
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1959
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (10)..(1572)
34 <220> FEATURE:
35 <221> NAME/KEY: MOD_RES
36 <222> LOCATION: (520)
37 <223> OTHER INFORMATION: Selenocysteine
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41 Met Ala Val Ala Leu Arg Gly Leu Gly Arg Phe Arg Trp
42 1 5 10
44 cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca 99
45 Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
46 15 20 25 30
48 gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct 147
49 Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Ser
50 35 40 45
52 ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg 195
53 Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
54 50 55 60
56 gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc 243
57 Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
58 65 70 75
60 ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg 291
61 Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
62 80 85 90
64 cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat 339
65 His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr
66 95 100 105 110
68 ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca 387

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69	Gly	Trp	Glu	Val	Ala	Gln	Pro	Val	Pro	His	Asp	Trp	Arg	Lys	Met	Ala	
70				115					120						125		
72	gaa	gct	gtt	caa	aat	cac	gtg	aaa	tcc	ttg	aac	tgg	ggc	cac	cgt	gtc	435
73	Glu	Ala	Val	Gln	Asn	His	Val	Lys	Ser	Leu	Asn	Trp	Gly	His	Arg	Val	
74				130					135						140		
76	cag	ctt	cag	gac	aga	aaa	gtc	aag	tac	ttt	aac	atc	aaa	gcc	agc	ttt	483
77	Gln	Leu	Gln	Asp	Arg	Lys	Val	Lys	Tyr	Phe	Asn	Ile	Lys	Ala	Ser	Phe	
78				145					150						155		
80	gtt	gac	gag	cac	acg	gtt	tgc	ggc	gtt	gcc	aaa	gtt	ggg	aaa	gag	att	531
81	Val	Asp	Glu	His	Thr	Val	Cys	Gly	Val	Ala	Lys	Gly	Gly	Lys	Glu	Ile	
82				160			165			165					170		
84	ctg	ctg	tca	gcc	gat	cac	atc	atc	att	gct	act	gga	ggg	cg	aga		579
85	Leu	Leu	Ser	Ala	Asp	His	Ile	Ile	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Arg	
86	175			180					185						190		
88	tac	ccc	acg	cac	atc	gaa	ggt	gcc	ttg	gaa	tat	gga	atc	aca	agt	gat	627
89	Tyr	Pro	Thr	His	Ile	Glu	Gly	Ala	Leu	Glu	Tyr	Gly	Ile	Thr	Ser	Asp	
90				195					200						205		
92	gac	atc	tcc	tgg	ctg	aag	gaa	tcc	cct	gga	aaa	acg	ttg	gtg	gtc	ggg	675
93	Asp	Ile	Phe	Trp	Leu	Lys	Glu	Ser	Pro	Gly	Lys	Thr	Leu	Val	Val	Gly	
94				210					215						220		
96	gcc	agc	tat	gtg	gcc	ctg	gag	tgt	gct	ggc	ttc	ctc	acc	ggg	att	ggg	723
97	Ala	Ser	Tyr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Thr	Gly	Ile	Gly	
98				225			230			230					235		
100	ctg	gac	acc	acc	atc	atc	atg	cgc	agc	atc	ccc	ctc	cgc	ggc	ttc	gac	771
101	Leu	Asp	Thr	Thr	Ile	Met	Met	Arg	Ser	Ile	Pro	Leu	Arg	Gly	Phe	Asp	
102				240			245			245					250		
104	cag	caa	atg	tcc	tcc	atg	gtc	ata	gag	cac	atg	gca	tct	cat	ggc	acc	819
105	Gln	Gln	Met	Ser	Ser	Met	Val	Ile	Glu	His	Met	Ala	Ser	His	Gly	Thr	
106	255				260				265						270		
108	cgg	ttc	ctg	agg	ggc	tgt	gcc	ccc	tcg	cg	agg	gg	ctc	cct	gat		867
109	Arg	Phe	Leu	Arg	Gly	Cys	Ala	Pro	Ser	Arg	Val	Arg	Arg	Leu	Pro	Asp	
110				275					280						285		
112	ggc	cag	ctg	cag	gtc	acc	tgg	gag	gac	agc	acc	acc	ggc	aag	gag	gac	915
113	Gly	Gln	Leu	Gln	Val	Thr	Trp	Glu	Asp	Ser	Thr	Thr	Gly	Lys	Glu	Asp	
114				290					295						300		
116	acg	ggc	acc	ttt	gac	acc	gtc	ctg	tgg	gcc	ata	ggt	cga	gtc	cca	gac	963
117	Thr	Gly	Thr	Phe	Asp	Thr	Val	Leu	Trp	Ala	Ile	Gly	Arg	Val	Pro	Asp	
118				305			310			310					315		
120	acc	aga	agt	ctg	aat	ttg	gag	aag	gct	ggg	gta	gat	act	agc	ccc	gac	1011
121	Thr	Arg	Ser	Leu	Asn	Leu	Glu	Lys	Ala	Gly	Val	Asp	Thr	Ser	Pro	Asp	
122				320			325			325					330		
124	act	cag	aag	atc	ctg	gtg	gac	tcc	cg	gaa	gcc	acc	tct	gtg	ccc	cac	1059
125	Thr	Gln	Lys	Ile	Leu	Val	Asp	Ser	Arg	Glu	Ala	Thr	Ser	Val	Pro	His	
126	335				340				345						350		
128	atc	tac	gcc	att	ggt	gac	gtg	gtg	gag	ggg	cg	cct	gag	ctg	aca	ccc	1107
129	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Val	Glu	Gly	Arg	Pro	Glu	Leu	Thr	Pro	
130				355					360						365		
132	aca	gcg	atc	atg	gcc	ggg	agg	ctc	ctg	gtg	cag	cg	ctc	tcc	ggc	ggg	1155
133	Thr	Ala	Ile	Met	Ala	Gly	Arg	Leu	Leu	Val	Gln	Arg	Leu	Phe	Gly	Gly	

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134	370	375	380	
136	tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc			1203
137	Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr			
138	385	390	395	
140	cca ctg gag tat ggc tgt ggg ctg tcc gag gag gag gca gtg gct			1251
141	Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Ala Val Ala			
142	400	405	410	
144	cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca			1299
145	Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro			
146	415	420	425	430
148	ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag			1347
149	Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys			
150	435	440	445	
152	atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc			1395
153	Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe			
154	450	455	460	
156	ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc			1443
157	Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile			
158	465	470	475	
160	aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat			1491
161	Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His			
162	480	485	490	
164	ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca			1539
165	Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser			
166	495	500	505	510
168	ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc			1592
W-->169	Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly			
170	515	520		
172	cagggcacac ggtgcgccccg ccgccagctc ctcggaggcc agacccagga tggctgcagg			1652
174	ccaggtttgg ggggcctcaa ccctctccctg gagccctgt gagatggta gcgtggagcg			1712
176	caagtgtgg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc			1772
178	acccctgcac cttcagcct ttgcccggc gcacccccc caggctcctg gtgcccgtg			1832
180	atgacgaccc ggggtggaaac ctaccctgtg ggcacccatg tccgagcccc ctgcatttc			1892
182	tgcaatgcaa ataaagaggg tacttttct gaagtgtgt aaaaaaaaaaaaaaaa			1952
184	aaaaaaaa			1959
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188	<211> LENGTH: 521			
189	<212> TYPE: PRT			
190	<213> ORGANISM: Homo sapiens			
192	<220> FEATURE:			
193	<221> NAME/KEY: MOD_RES			
194	<222> LOCATION: (520)			
195	<223> OTHER INFORMATION: Selenocysteine			
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201	Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala Ala Ala			
202	20	25	30	
204	Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Ser Gly Gly			

protein
identified in a
DNA sequence
OK

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205	35	40	45	
207	Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val			
208	50	55	60	
210	Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly			
211	65	70	75	80
213	Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln			
214	85	90	95	
216	Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp			
217	100	105	110	
219	Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala			
220	115	120	125	
222	Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu			
223	130	135	140	
225	Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp			
226	145	150	155	160
228	Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu			
229	165	170	175	
231	Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro			
232	180	185	190	
234	Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile			
235	195	200	205	
237	Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser			
238	210	215	220	
240	Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp			
241	225	230	235	240
243	Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln			
244	245	250	255	
246	Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe			
247	260	265	270	
249	Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln			
250	275	280	285	
252	Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly			
253	290	295	300	
255	Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg			
256	305	310	315	320
258	Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln			
259	325	330	335	
261	Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr			
262	340	345	350	
264	Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala			
265	355	360	365	
267	Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser			
268	370	375	380	
270	Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu			
271	385	390	395	400
273	Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His			
274	405	410	415	
276	Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu			
277	420	425	430	

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279 Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
280 435 440 445
282 Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
283 450 455 460
285 Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
286 465 470 475 480
288 Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
289 485 490 495
291 Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu
292 500 505 510

W--> 294 Asp Pro Thr Val Thr Gly Cys (Xaa) Gly ✓
295 515 520

298 <210> SEQ ID NO: 3
299 <211> LENGTH: 2056
300 <212> TYPE: DNA
301 <213> ORGANISM: Homo sapiens
303 <220> FEATURE:
304 <221> NAME/KEY: CDS
305 <222> LOCATION: (188)..(1669)
307 <220> FEATURE:
308 <221> NAME/KEY: MOD_RES
309 <222> LOCATION: (493)
310 <223> OTHER INFORMATION: Selenocysteine
312 <400> SEQUENCE: 3
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315 ttctccatcc ctccctttt tggctgccc ttgcctgcct tcctcgccag tagcttgcag 120
317 agtagacacg atgacacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180
319 agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229
320 Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
321 1 5 10
323 gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gca cag 277
324 Val Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
325 15 20 25 30
327 ctg gga agg aag gtg gcc gtg gac tac gtg gaa cct tct ccc caa 325
328 Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
329 35 40 45
331 ggc acc cgg tgg ggc ctc ggc acc tgc gtc aac gtg ggc tgc atc 373
332 Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
333 50 55 60
335 ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa 421
336 Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
337 65 70 75
339 gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac 469
340 Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
341 80 85 90
343 tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac 517
344 Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
345 95 100 105 110
347 tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac 565

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\55871965.app

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L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:2002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38